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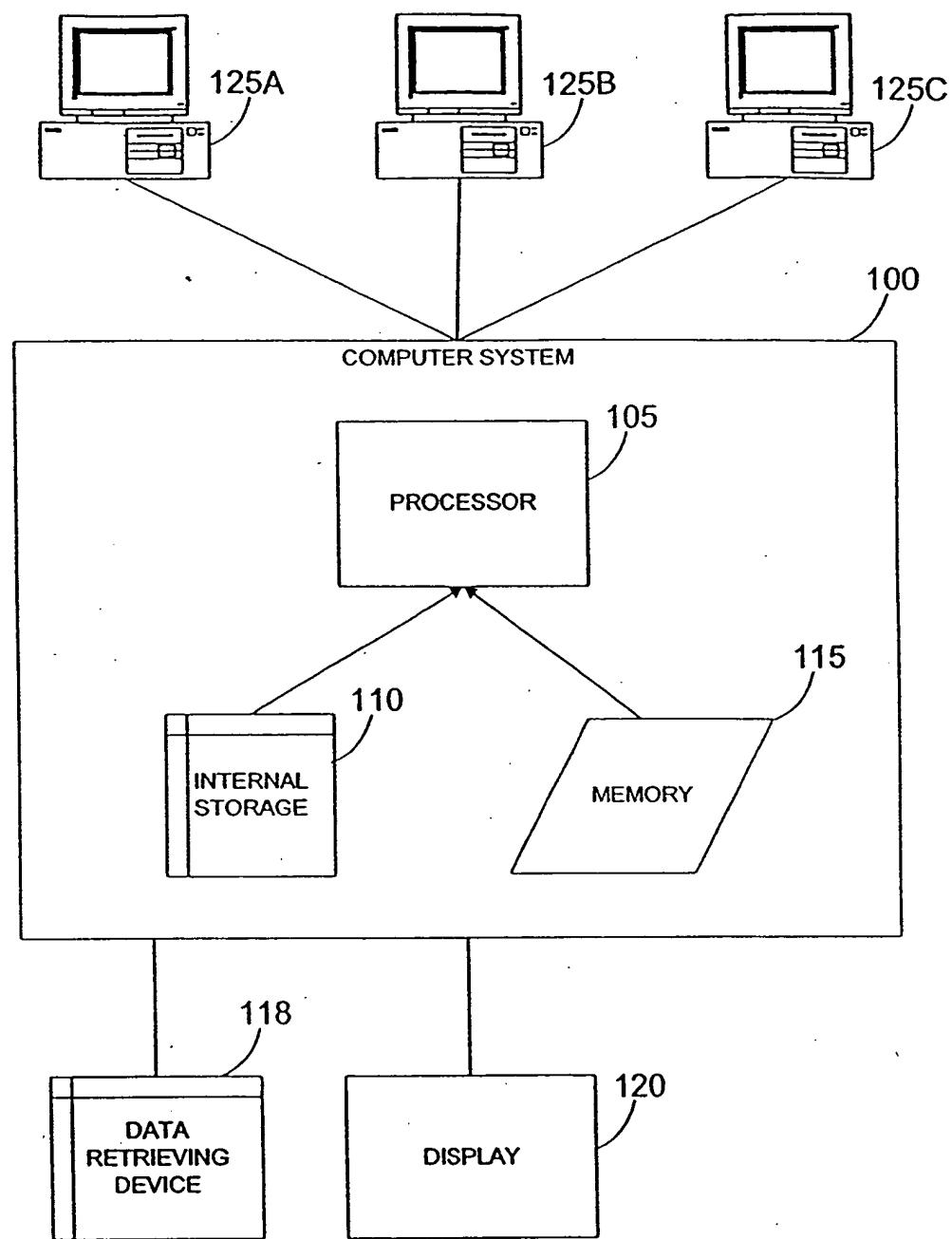


FIGURE 1

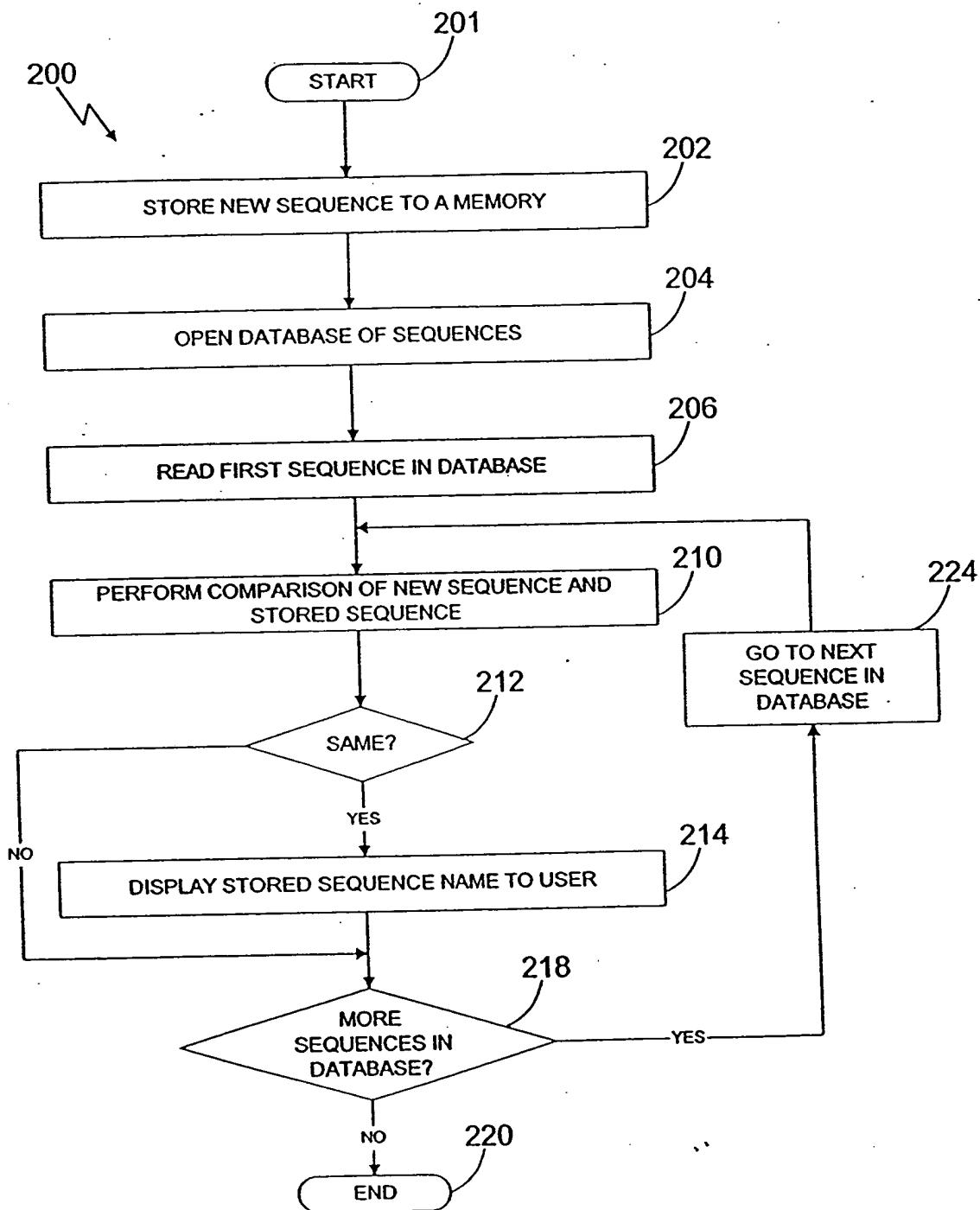


FIGURE 2

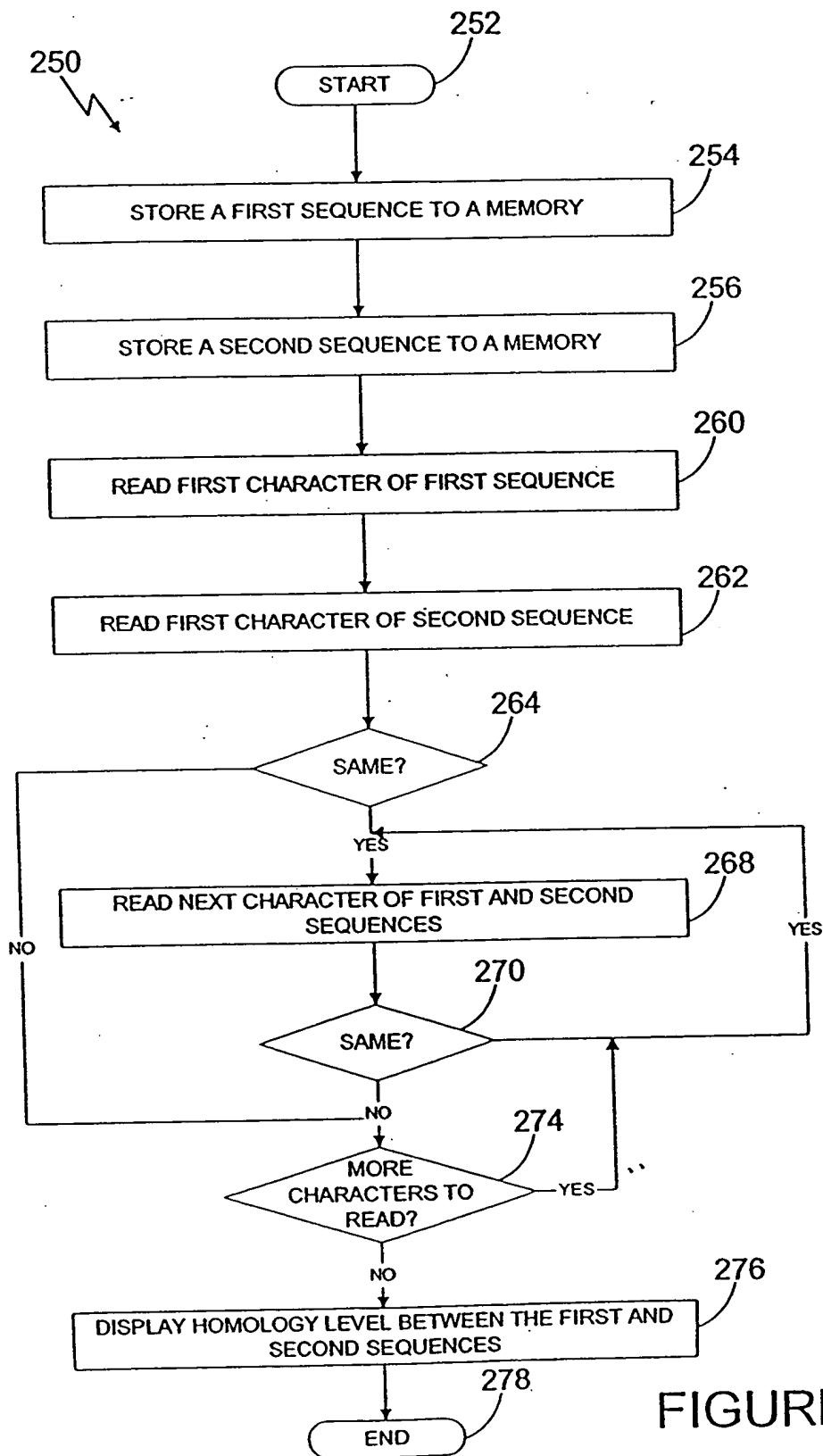


FIGURE 3

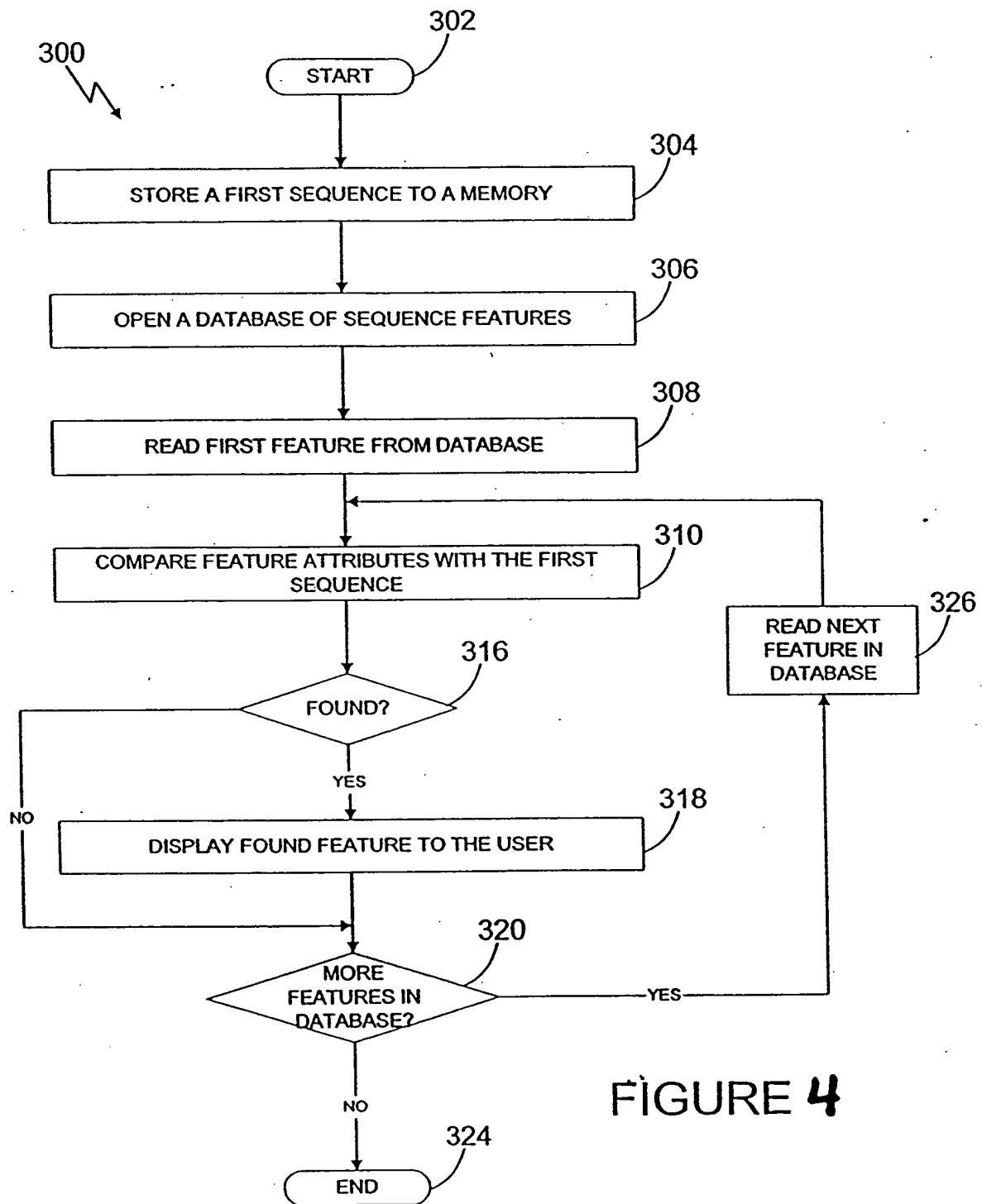


FIGURE 4

# FIGURE 5

## Ammonifex degensii KC4 Phosphatase (3A1A=3A2A) Complete gene sequence

ATGAGGGGGAGCGGAGTCGGATACTTCTCACCAACGATGACGGCATCTTGCCGAGGGT  
1 MetArgGlySerGlyValArgIleLeuLeuThrAsnAspAspGlyIlePheAlaGluGly  
  
CTGGGGGCTCTCGCAAGATGCTGGAGCCCGTGGCTACCCCTTACGTGGTGGCTCCGGAC  
21 LeuGlyAlaLeuArgLysMetLeuGluProValAlaThrLeuTyrValValAlaProAsp  
  
CGAGAGCGTAGCGCGGCCAGCCATGCTATCACCGTTCACCGCCCCCTGCCGGTGGGGAG  
41 ArgGluArgSerAlaAlaSerHisAlaIleThrValHisArgProLeuArgValArgGlu  
  
GCGGGTTTCGCAGCCCCAGGCTAAAGGCTGGGTAGTGGACGGTACCCCGGCCACTGC  
61 AlaGlyPheArgSerProArgLeuLysGlyTrpValValAspGlyThrProAlaAspCys  
  
GTCAAGCTGGGCCTGGAGGTACTTTGCCGAACGTCCAGATTCTGGTTCTGGGCATA  
81 ValLysLeuGlyLeuGluValLeuLeuProGluArgProAspPheLeuValSerGlyIle  
  
AACTACGGGCCAACCTGGGTACCGACGTACTTACTCCGGCACCGTCTGGCGGCCATA  
101 AsnTyrGlyProAsnLeuGlyThrAspValLeuTyrSerGlyThrValSerAlaAlaIle  
  
GAAGGGTAATTAAACGGCATTCCCTCGTGGCCGTATCTTGCCACGCCGGAGCCG  
121 GluGlyValIleAsnGlyIleProSerValAlaValSerLeuAlaThrArgArgGluPro  
  
GACTATACTGGCGGCCGGTTCGTCTGGCCTGCTGGAGGAACCGCGAAAACACCAA  
141 AspTyrThrTrpAlaAlaArgPheValLeuValLeuGluLeuArgLysHisGln  
  
CTGCCCCCAGGAACCTGCTAACGTCAACGTGCCGACGGGTGCCCGCGGGTCAAG  
161 LeuProProGlyThrLeuLeuAsnValAsnValProAspGlyValProArgGlyValLys  
  
GTGACCAAACTGGGAAGCGTACGCTACGTCAACGTGGTAGACTGCCGACCGACCCCTCGG  
181 ValThrLysLeuGlySerValArgTyrValAsnValValAspCysArgThrAspProArg  
  
GGGAAGGCTTACTACTGGATGGCGGGAGAACATTGGAGCTGGACGGCAACGACTCCGAA  
201 GlyLysAlaTyrTyrTrpMetAlaGlyGluProLeuGluLeuAspGlyAsnAspSerGlu  
  
ACCGACGTCTGGCGGTGCGAGAACGGCTATATTCGTAACACCGGTCCAGATCGACCTT  
221 ThrAspValTrpAlaValArgGluGlyTyrIleSerValThrProValGlnIleAspLeu  
  
ACTAACTACGGCTTCCTGGAAGAACCTAAAAATGGCGTTCAAGGATATCTTTCTTCT  
241 ThrAsnTyrGlyPheLeuGluGluLeuLysLysTrpArgPheLysAspIlePheSerSer  
  
TAA  
261 End 261

# FIGURE 6

## *Methanococcus igneus* Ko15 Phosphatase (9A1A) Complete Gene Sequence

ATGTTGGATATACTGCTGTTATGATGATGGCATTATTCAAATGGATTAATAGCTTTG  
1 MetLeuAspIleLeuLeuValAsnAspAspGlyIleTyrSerAsnGlyLeuIleAlaLeu  
  
AAGGATGCATTATTGGAAAAATTAAATGCGAGGATTACTATTGTAGCCCCAACAAATCAG  
21 LysAspAlaLeuLeuGluLysPheAsnAlaArgIleThrIleValAlaProThrAsnGln  
  
CAGAGTGGTATTGGTAGGGCAATAAGTTATTGAGCCGTTAAGGATAACTAAAACCAAA  
41 GlnSerGlyIleGlyArgAlaIleSerLeuPheGluProLeuArgIleThrLysThrLys  
  
TTAGCAGATGGTTCTGGGGATATGCAGTTTCAGGAACCCAACAGATTGCGTTATATTG  
61 LeuAlaAspGlySerTrpGlyTyrAlaValSerGlyThrProThrAspCysValIleLeu  
  
GGCATTATGAGATATTAAAGAAGGTACCTGATGTAGTTATATCAGGAATAAACATTGGA  
81 GlyIleTyrGluIleLeuLysLysValProAspValValIleSerGlyIleAsnIleGly  
  
GAAAACCTTGGGACTGAAATAACAACTTCTGGAACGTTGGGGCTGCGTTGAAGGGGCC  
101 GluAsnLeuGlyThrGluIleThrSerGlyThrLeuGlyAlaAlaPheGluGlyAla  
  
CATCATGGGCTAACGCATTAGCATCATCACTCCAAGTTACCTCTGACCATCTAAAGTTT  
121 HisHisGlyAlaLysAlaLeuAlaSerSerLeuGlnValThrSerAspHisLeuLysPhe  
  
AAAGAGGGGGAGACCCCAATAGACTTCACAGTCCAGCAAGAATTACTGCAAATGTTGTT  
141 LysGluGlyGluThrProIleAspPheThrValProAlaArgIleThrAlaAsnValVal  
  
GAGAAGATGTTGGATTATGATTCCCATGTGATGTCGTCAACTAAACATTCCAGAAGGA  
161 GluLysMetLeuAspTyrAspPheProCysAspValValAsnLeuAsnIleProGluGly  
  
GCAACAGAAAAGACACCGATTGAAATCACAGGTTGGCAAGGAAATGTATACAACACAC  
181 AlaThrGluLysThrProIleGluIleThrArgLeuAlaArgLysMetTyrThrThrHis  
  
GTTGAGGAAAGAATAGATCCAAGAGGGAGGAGTTATTATTGGATTGATGGGTATCCTATT  
201 ValGluGluArgIleAspProArgGlyArgSerTyrTyrTrpIleAspGlyTyrProIle  
  
TTAGAGGAAGAGGAAGACACTGATGTCTATGTTGTTAGAAGAAAGGGACATATTCTCTA  
221 LeuGluGluGluAspThrAspValTyrValValArgArgLysGlyHisIleSerLeu  
  
ACCCCATTAACATTAGACACAACAATTAAAATTAGAGGAATTAAAGAAAAATATGAG  
241 ThrProLeuThrLeuAspThrThrIleLysAsnLeuGluGluPheLysLysTyrGlu  
  
AGAATATTAAATGAATGA  
261 ArgIleLeuAsnGluEnd 266

# FIGURE 7

## *Thermococcus alcaliphilus AEDII12RA Phosphatase (18A)* Complete Gene Sequence

1 ATGATGATGGAATTCACTCGCGAGGGAAATAAAAGCTGCTGTAGAGGCACCTCAAGGGTTA  
MetMetMetGluPheThrArgGluGlyIleLysAlaAlaValGluAlaLeuGlnGlyLeu

21 GGAGAGATCTACGTAGTTGCCCAATGTTCAAAGGAGCGCAAGTGGAAAGGGCAATGACC  
GlyGluIleTyrValValAlaProMetPheGlnArgSerAlaSerGlyArgAlaMetThr

41 ATCCACAGACCTCTAAGGGCTAAAAGAATAAGTATGAACGGTGCAAAAGCAGCCTATGCT  
IleHisArgProLeuArgAlaLysArgIleSerMetAsnGlyAlaLysAlaAlaTyrAla

61 TTGGATGGAATGCCGTTGATTGCGTTATCTTGCCATGCCAGATTGGAGATTCGAC  
LeuAspGlyMetProValAspCysValIlePheAlaMetAlaArgPheGlyAspPheAsp

81 CTTGCAATAAGTGGTGTAAACTTGGGAGAAAACATGAGCACCGAGATAACGGTTCCGGG  
LeuAlaIleSerGlyValAsnLeuGlyGluAsnMetSerThrGluIleThrValSerGly

101 ACTGCAAGCGCTGCAATAGAGGCTGCAACCCAAGAGATCCCAAGCATTCCCATAAGCCTG  
ThrAlaSerAlaAlaIleGluAlaAlaThrGlnGluIleProSerIleProIleSerLeu

121 GAAGTTAATAGAGAAAAACACAAATTGGTGAGGGCGAAGAGATTGACTTCTCAGCTGCC  
GluValAsnArgGluLysHisLysPheGlyGluGlyGluIleAspPheSerAlaAla

141 AAGTATTCCTAAGAAAAATCGCAACGGCGTTAAAGAGAGGCCCTCCCAAAGGAGTC  
LysTyrPheLeuArgLysIleAlaThrAlaValLeuLysArgGlyLeuProLysGlyVal

161 GATATGCTAACGTCAACGTCCCTTATGATGCAAATGAAAGGACAGAGATAGCTTTACT  
AspMetLeuAsnValAsnValProTyrAspAlaAsnGluArgThrGluIleAlaPheThr

181 CGCCTGGCAAGAAGGATGTATAGGCCTTCTATTGAAGAGCGCATAGACCCAAAGGGAAAT  
ArgLeuAlaArgArgMetTyrArgProSerIleGluGluArgIleAspProLysGlyAsn

201 CCCTACTACTGGATAGTTGGAACTCAGTGCCTAAGGAGGCATTAGAGCCGGAACGGAT  
ProTyrTyrTrpIleValGlyThrGlnCysProLysGluAlaLeuGluProGlyThrAsp

221 ATGTATGTAGTTAAAGTTGAGAGAAAAGTTAGCGTGACTCCAATAAACATTGATATGACA  
MetTyrValValLysValGluArgLysValSerValThrProIleAsnIleAspMetThr

241 GCAAGAGTGAATTAGACCGAGATTAAAAGACTTTAGAACTGTAG  
AlaArgValAsnLeuAspGluIleLysArgLeuLeuGluLeuEnd 255

## FIGURE 8

### *Thermococcus celer* Phosphatase (25A1A) Complete Gene Sequence

|     |  |     |
|-----|--|-----|
| 1   | ATGAGAACCTGACAATAAACACTGACGGAGGGGTCGTTTGAGGATTCTCCTGACG<br>MetArgThrLeuThrIleAsnThrAspAlaGluGlyPheValLeuArgIleLeuLeuThr        | 20  |
| 21  | AACGACGATGGAATCTACTCCAACGGACTGCGCGCCGCTGTGAAAGCCCTGAGTGAGCTC<br>AsnAspAspGlyIleTyrSerAsnGlyLeuArgAlaAlaValLysAlaLeuSerGluLeu   | 40  |
| 41  | GGCGAAGTTACGTCTGCCCTCTTCCAGAGGAGCGCGAGCGGAGGGCCATGACG<br>GlyGluValTyrValValAlaProLeuPheGlnArgSerAlaSerGlyArgAlaMetThr          | 60  |
| 61  | CTCCACAGGCCATAAGGGCCAAGCGCGTTGACGTTCCCGCGCAAAGATAAGCCTACGGA<br>LeuHisArgProIleArgAlaLysArgValAspValProGlyAlaLysIleAlaTyrGly    | 80  |
| 81  | ATAGATGGAACCTCTACTGACTGCGTGATTTGCCATAGCCCGCTTCGGGAGCTTG<br>IleAspGlyThrProThrAspCysValIlePheAlaIleAlaArgPheGlySerPheGly        | 100 |
| 101 | TTAGCCGTGAGCGGGATTAAACCTCGCGAGAACCTGAGCACCGAGATAACAGTCTCAGGG<br>LeuAlaValSerGlyIleAsnLeuGlyGluAsnLeuSerThrGluIleThrValSerGly   | 120 |
| 121 | ACGGCCTCCGCTGCCATAGAGGCCTCAACTCATGGAATTCCGAGCATAGCGATTAGCCTT<br>ThrAlaSerAlaAlaIleGluAlaSerThrHisGlyIleProSerIleAlaIleSerLeu   | 140 |
| 141 | GAGGTGGAGTGAAGAACGACCTCGCGAGGGTGAGGGGGTTGACTTCTCGGTCTGACT<br>GluValGluTrpLysLysThrLeuGlyGluGlyGluGlyValAspPheSerValSerThr      | 160 |
| 161 | CACTCCTCAAGAGAACGCGGGAGCCCTCTTGGAGAGAGGTCTCCTGAGGGCGTTGAC<br>HisPheLeuLysArgIleAlaGlyAlaLeuLeuGluArgGlyLeuProGluGlyValAsp      | 180 |
| 181 | ATGCTAACGTCAACGTTCCGAGCGACCGGACGGAGGAAACGGAGATAGCAATCACCCGC<br>MetLeuAsnValAsnValProSerAspAlaThrGluGluThrGluIleAlaIleThrArg    | 200 |
| 201 | TTAGCCCGGAAGCGCTACTCCCCAACGGTCGAGGAGAGGATTGACCCCAAGGGCAACCCC<br>LeuAlaArgLysArgTyrSerProThrValGluGluArgIleAspProLysGlyAsnPro   | 220 |
| 221 | TACTACTGGATTGTCGGCAAACCTGTCCAAGACTTCGAGGCCAGGGACAGATGCCCTACGCC<br>TyrTyrTrpIleValGlyLysLeuValGlnAspPheGluProGlyThrAspAlaTyrAla | 240 |
| 241 | CTGAAGGTCGAGAGGAAGGTCAGCGTCACGCCATAAACATAGATATGACTGCGAGGGTG<br>LeuLysValGluArgLysValSerValThrProIleAsnIleAspMetThrAlaArgVal    | 260 |
| 261 | GAATTGAGGAGCTTGTAAGGGTTCTGTGGGTGAA<br>AspPheGluGluLeuValArgValLeuTrpValEnd   | 272 |

# FIGURE 9A

## *Thermococcus GU5L5* Phosphatase (26A1A) Complete Gene Sequence (Part 1 of 2)

|     |  |     |
|-----|--|-----|
| 1   | ATGAAAGGAAAGTCTTGTAGCGGTCTGGTGGGCTTTAATTTGAGCCTGATT<br>MetLysGlyLysSerLeuValSerGlyLeuLeuLeuGlyLeuLeuIleLeuSerLeuIle          | 20  |
| 21  | TCATTCCAGCCAAGCTTGCATACTCCCCACACGGCGGTGTCAAAAACATCATAATCCTG<br>SerPheGlnProSerPheAlaTyrSerProHisGlyGlyValLysAsnIleIleIleLeu  | 40  |
| 41  | GTTGGAGACGGCATGGCTTGGGCATGTAGAAATTACAAAGCTCGTTATGGACACTTA<br>ValGlyAspGlyMetGlyLeuGlyHisValGluIleThrLysLeuValTyrGlyHisLeu    | 60  |
| 61  | AACATGGAAAACTTCCAGTTACTGGATTGAGCTTACTGATTCCTAAGTGGTGAAGTT<br>AsnMetGluAsnPheProValThrGlyPheGluLeuThrAspSerLeuSerGlyGluVal    | 80  |
| 81  | ACAGATTCTGCTGCGCAGGAACGTGCAATATCCACTGGAGCTAAAACGTATAATGGTATG<br>ThrAspSerAlaAlaAlaGlyThrAlaIleSerThrGlyAlaLysThrTyrAsnGlyMet | 100 |
| 101 | ATTTCACTAACATAACCGGAAAGATAGTTAACAAACCCCTACTTGAAGTGGCT<br>IleSerValThrAsnIleThrGlyLysIleValAsnLeuThrThrLeuLeuGluValAla        | 120 |
| 121 | CAAGAGCTTGGGAAACTCAACAGGGCTGGTCACCACAACAAGGATTACCCATGCAAACCTCA<br>GlnGluLeuGlyLysSerThrGlyLeuValThrThrArgIleThrHisAlaThrPro  | 140 |
| 141 | GCAGTTTGTGCTCCATGTCCCAGATAGGGATATGGAGGGGAGATACCCAACCAAAC<br>AlaValPheAlaSerHisValProAspArgAspMetGluGlyGluIleProLysGlnLeu     | 160 |
| 161 | ATAATGCACAAAGTTAACGTCTTGTGGTGGTGGAAAGGGAGAAATTGATGAGAAAAAT<br>IleMetHisLysValAsnValLeuLeuGlyGlyArgGluLysPheAspGluLysAsn      | 180 |
| 181 | TTGGAGCTGGCAAAAGCAGGGATACAAAGTAGTTTACCGAAGGAAGAGCTTGAAAAA<br>LeuGluLeuAlaLysLysGlnGlyTyrLysValValPheThrLysGluGluLeuGluLys    | 200 |
| 201 | GTTGAAGGAGATTATGCTCTAGGACTCTTGCAGAAAGTCACATCCCTTACGTATTGGAT<br>ValGluGlyAspTyrValLeuGlyLeuPheAlaGluSerHisIleProTyrValLeuAsp  | 220 |
| 221 | AGAAAACCCGATGATGTTGGACTTTAGAAATGGCAAAAGGCAATTCAATACTCGAG<br>ArgLysProAspAspValGlyLeuLeuGluMetAlaLysLysAlaIleSerIleLeuGlu     | 240 |
| 241 | AAGAACCCGAGCGGATTCTTCTCATGGTTGAGGGCGGAAGGATTGACCATGCGCCAT<br>LysAsnProSerGlyPhePheLeuMetValGluGlyGlyArgIleAspHisAlaAlaHis    | 260 |
| 261 | GGAAACGATGTCGCATGGTTGTCAGAAACTAAGGAGTTGACGATGTTGTCAGATA<br>GlyAsnAspValAlaSerValValAlaGluThrLysGluPheAspAspValValArgTyr      | 280 |
| 281 | GTGCTGGAATATCCGAAGAAGAGGGGAGATACCTTGGTAATAGTGCTTGCGATCACGAA<br>ValLeuGluTyrProLysLysArgGlyAspThrLeuValIleValLeuAlaAspHisGlu  | 300 |
| 301 | ACTGGAGGTCTTGCATAGCTAACGATGGAAATGCAATCGATGAAGATGCCATAAGA<br>ThrGlyGlyLeuAlaIleGlyLeuThrTyrGlyAsnAlaIleAspGluAspAlaIleArg     | 320 |
| 321 | AAAATAAAAGCAAGCACGTTGACCATGCCAAAGAGGTTAAGGCAGGGAGTAGTGTAAAAA<br>LysIleLysAlaSerThrLeuArgMetProLysGluValLysAlaGlySerSerValLys | 340 |

# FIGURE 9B

## *Thermococcus GU5L5 Phosphatase (26A1A)* Complete Gene Sequence (Part 2 of 2)

|     |   |     |
|-----|---|-----|
|     | GAGTCCTCAAAGGTATGCCGGATTGTCCCAACAGAGGAAGAAGTCAGTATATTGAGAAT   |     |
| 341 | GluSerSerLysValCysArgIleCysProAsnArgGlyArgSerGlnTyrIleGluAsn  | 360 |
|     | GCGCTGCACTCGACAAACAAAGTATGCCCTCTCAAATGCAGTAGCCGATGTTATAAACAGG |     |
| 361 | AlaLeuHisSerThrAsnLysTyrAlaLeuSerAsnAlaValAlaAspValIleAsnArg  | 380 |
|     | CGTATTGGTGGATTCACCTCCTATGAGCATACAGGAGTTCCAGTCCGCTCTTAGCT      |     |
| 381 | ArgIleGlyValGlyPheThrSerTyrGluHisThrGlyValProValProLeuLeuAla  | 400 |
|     | TACGGTCCCAGGGCAGAGAACTTCAGAGGTTCTACACCAGTGGATACAGCAAGATT      |     |
| 401 | TyrGlyProGlyAlaGluAsnPheArgGlyPheLeuHisHisValAspThrAlaArgLeu  | 420 |
|     | GTTGCAAAGTTAATGCTCTTGGAAGGAGGAATATTCCAGTTACCAATTCAAGCGTGAGC   |     |
| 421 | ValAlaLysLeuMetLeuPheGlyArgArgAsnIleProValThrIleSerSerValSer  | 440 |
|     | AGTGTAAAGGGAGACATAACCGGTGATTACAGGGTGATGAGAAGGGATGCCTACGTTACG  |     |
| 441 | SerValLysGlyAspIleThrGlyAspTyrArgValAspGluLysAspAlaTyrValThr  | 460 |
|     | CTCATGATGTTCTCGGAGAAAAAGTGGATAATGAAATTGAAAAGAGAGTCGATATAGAC   |     |
| 461 | LeuMetMetPheLeuGlyGluLysValAspAsnGluIleGluLysArgValAspIleAsp  | 480 |
|     | AACAAACGGCATGGTGACTAAATGACGTCATGTTGATTCTCCAGGAAGCTTGA         |     |
| 481 | AsnAsnGlyMetValAspLeuAsnAspValMetLeuIleLeuGlnGluAlaEnd        | 498 |

# FIGURE 10A

## OC9a Phosphatase (27A3A) Complete Gene Sequence (Part 1 of 2)

|     |   |     |
|-----|---|-----|
| 1   | ATGCCAAGAAATATGCCGCTGTATGCCCTGGCCCTGGCCCTGGCG                 | 20  |
| 1   | MetProArgAsnIleAlaAlaValCysAlaLeuAlaAlaLeuLeuGlySerAlaTrpAla  |     |
| 21  | GCCAAAGTTGCCGCTTACCCCTACGACGGAGCCGTTGCTGGCGGGGCAGCGCTTCGAT    | 40  |
| 21  | AlaLysValAlaValTyrProTyrAspGlyAlaAlaLeuAlaGlyGlnArgPheAsp     |     |
| 41  | TTGCGCATAGAACGCCCTCGAGCTGAAAGGCAATTAAAGGCTTACCGCATCACCCCTGGAC | 60  |
| 41  | LeuArgIleGluAlaSerGluLeuLysGlyAsnLeuLysAlaTyrArgIleThrLeuAsp  |     |
| 61  | GGCCAGCCTCTGGCGGGCCTCGAGCAAACCGCGCAGGGGCCGGCAGGCCGAGTGGACC    | 80  |
| 61  | GlyGlnProLeuAlaGlyLeuGluGlnThrAlaGlnGlyAlaGlyGlnAlaGluTrpThr  |     |
| 81  | CTGCGCGGTGCCTTCCTGCGCCCTGGAAGCCACACCCCTCGAGGTCAGCCTCACGACGAC  | 100 |
| 81  | LeuArgGlyAlaPheLeuArgProGlySerHisThrLeuGluValSerLeuThrAspAsp  |     |
| 101 | GCTGGGGAGAGCAGGAAGAGCGTACGTTGGAGGCTCGGCAGAACCTTCGCTTGCCCCGA   | 120 |
| 101 | AlaGlyGluSerArgLysSerValArgTrpGluAlaArgGlnAsnLeuArgLeuProArg  |     |
| 121 | GCGGCCAAGAATGTGATTCTCTTCATTGGCGACGGGATGGGCTGGAACACCCCTCAACGCC | 140 |
| 121 | AlaAlaLysAsnValIleLeuPheIleGlyAspGlyMetGlyTrpAsnThrLeuAsnAla  |     |
| 141 | GCCCGCATCATGCCAAAGGCTTAACCCGAAACGGTATGCCAACGGAAACCTCGAG       | 160 |
| 141 | AlaArgIleIleAlaLysGlyPheAsnProGluAsnGlyMetProAsnGlyAsnLeuGlu  |     |
| 161 | ATCGAGAGTGGTTACGGTGGGATGGCTACCGTCACTACCGGCAGCTTGATAGCTTCATC   | 180 |
| 161 | IleGluSerGlyTyrGlyGlyMetAlaThrValThrThrGlySerPheAspSerPheIle  |     |
| 181 | GCCGACTCAGCTAACTCGGCTCTTCCATCATGACCGGGCAGAAGGTGCAGGTGAATGCC   | 200 |
| 181 | AlaAspSerAlaAsnSerAlaSerSerIleMetThrGlyGlnLysValGlnValAsnAla  |     |
| 201 | CTCAACGTTTACCCATCAAACCTCAAAGATAACCTGGCTACCCCGGATCGAAACCCCTA   | 220 |
| 201 | LeuAsnValTyrProSerAsnLeuLysAspThrLeuAlaTyrProArgIleGluThrLeu  |     |
| 221 | GCGGAGATGCTCAAGCGGGTACCGGGGGCCAGCATGGGCTAGTGACCAACCACCTCGGC   | 240 |
| 221 | AlaGluMetLeuLysArgValArgGlyAlaSerIleGlyValValThrThrPheGly     |     |
| 241 | ACCGACGCTACCCCGGTTCACTCAACGCCATACCCGCCGCCGGTGATTACCAAGGCT     | 260 |
| 241 | ThrAspAlaThrProAlaSerLeuAsnAlaHisThrArgArgGlyAspTyrGlnAla     |     |
| 261 | ATCGCCGACATGTACTTGGTAGAGGGGGTCGGTGTCCCTGGATGTGATGCTCTTC       | 280 |
| 261 | IleAlaAspMetTyrPheGlyArgGlyGlyPheGlyValProLeuAspValMetLeuPhe  |     |
| 281 | GGTGGTTACCGCAGTCATCCCCAGAGCACCCCTGGCTCGCGCGCAAGGATAGCACG      | 300 |
| 281 | GlyGlySerArgAspPheIleProGlnSerThrProGlySerArgArgLysAspSerThr  |     |
| 301 | GACTGGATTGCCGAATCCCAGAGCTGGCTACACCTTGTCAGCACCCGAGCGAGCTG      | 320 |
| 301 | AspTrpIleAlaGluSerGlnLysLeuGlyTyrThrPheValSerThrArgSerGluLeu  |     |
| 321 | CTGGCGGGCAAACCCACCGATAAGCTTGGCTGTTCAACATTGACAACATTCCCCAGC     | 340 |
| 321 | LeuAlaAlaLysProThrAspLysLeuPheGlyLeuPheAsnIleAspAsnPheProSer  |     |

# FIGURE 10B

## OC9a Phosphatase (27A3A) Complete Gene Sequence (Part 2 of 2)

|     |  |     |
|-----|--|-----|
| 341 | TACCTAGACCGCCAGTGTGGAAGCGCCCGAGATGCTGGGAAGCTTTACCGATATGCC<br>TyrLeuAspArgAlaValTrpLysArgProGluMetLeuGlySerPheThrAspMetPro    | 360 |
| 361 | TACCTCTGGGAGATGACCCAGAAAGCCGTGGAGGCTCTCTCCAGAAACGACAAGGCTT<br>TyrLeuTrpGluMetThrGlnLysAlaValGluAlaLeuSerArgAsnAspLysGlyPhe   | 380 |
| 381 | TTCTTGATGGTTGAGGGGGAAATGGTGGATAAGTACGAGCACCCCTGGACTGGCCCCGC<br>PheLeuMetValGluGlyGlyMetValAspLysTyrGluHisProLeuAspTrpProArg  | 400 |
| 401 | GCACCTTGGGATGTACTCGAGCTGGACCGCGCGGTGGCTGGCCAAGGGCTATGCGGCC<br>AlaLeuTrpAspValLeuGluLeuAspArgAlaValAlaTrpAlaLysGlyTyrAlaAla   | 420 |
| 421 | TCCCACCCGATAACCTGGTATTGTCACCGCCGACCACGCTCACTCGATCTCGGTGTTT<br>SerHisProAspThrLeuValIleValThrAlaAspHisAlaHisSerIleSerValPhe   | 440 |
| 441 | GGCGGTTACGACTACTCCAAGCAGGGCCGGAGGGGGTGGGGGTTATGAGGCCGCCAAG<br>GlyGlyTyrAspTyrSerLysGlnGlyArgGluGlyValGlyValTyrGluAlaAlaLys   | 460 |
| 461 | TTCCCCACCTACGGCGACAAAAAGACGCCAACGGCTTCCCTGCCGACACCACTCGG<br>PheProThrTyrGlyAspLysLysAspAlaAsnGlyPheProLeuProAspThrThrArg     | 480 |
| 481 | GGAATCCGGTAGGCTTCGGGCCACGCCGGATTACTGTGAAACCTACCGGGGCCGAG<br>GlyIleAlaValGlyPheGlyAlaThrProAspTyrCysGluThrTyrArgGlyArgGlu     | 500 |
| 501 | GTCTACAAAGACCCCACCATCTCGACGGCAAAGGTGGTTACGTGGCCAACCCCTGAGGTC<br>ValTyrLysAspProThrIleSerAspGlyLysGlyGlyTyrValAlaAsnProGluVal | 520 |
| 521 | TGCAAGGAGCCGGCCTCCAACGTACCGCAACTCCCAGTAGATAGCGCCCAGGGCGTG<br>CysLysGluProGlyLeuProThrTyrArgGlnLeuProValAspSerAlaGlnGlyVal    | 540 |
| 541 | CACACGGCTGATCCCATGCCCTGTTGCCCTTGGCGTGGGTCTCAGTTCTCAATGGC<br>HisThrAlaAspProMetProLeuPheAlaPheGlyValGlySerGlnPhePheAsnGly     | 560 |
| 561 | CTCATCGACCAGACCGAGATCTTCCGCATGGCCCAGGCCCTAGGGTTCAACCCCCAC<br>LeuIleAspGlnThrGluIlePhePheArgMetAlaGlnAlaLeuGlyPheAsnProHis    | 580 |
| 581 | CTCGAGAAGCCTTAA<br>LeuGluLysProEnd 585   |     |

# FIGURE //

## M11 TL Phosphatase (29A1A=29A2A) Complete Gene Sequence

|     |   |     |
|-----|---|-----|
| 1   | ATGTATAAATGGATTATTGAGGGTAAGCTTGCCCAAGCACCTTCCAAGCCTAGGTGAA            | 20  |
| 1   | MetTyrLysTrpIleIleGluGlyLysLeuAlaGlnAlaProPheProSerLeuGlyGlu          |     |
| 21  | CTAGCCGATCTCAAAAGACTTTGACGCCATTATTGTTCTTACAATGCCGCATGAACAA            | 40  |
| 21  | LeuAlaAspLeuLysArgLeuPheAspAlaIleIleValLeuThrMetProHisGluGln          |     |
| 41  | CCGCTTAATGAGAAATATATCGAGATATTAGAGAGCCATGGATTCCAAGTCCTCCATGTC          | 60  |
| 41  | ProLeuAsnGluLysTyrIleGluIleLeuGluSerHisGlyPheGlnValLeuHisVal          |     |
| 61  | CCCACGCTCGACTTTCATCCTTAGAACTCTTCGACCTTTGAAAACAAGCATATTCAATT           | 80  |
| 61  | ProThrLeuAspPheHisProLeuGluLeuPheAspLeuLysThrSerIlePheIle             |     |
| 81  | GATGAAAACCTGGAGAGATCCCACAGAGTGCTTGCTTCACTGCATGGGAGGCATAGGCCGG         | 100 |
| 81  | AspGluAsnLeuGluArgSerHisArgValLeuValHisCysMetGlyGlyIleGlyArg          |     |
| 101 | AGCGGGCTTGTAAGTGCCTGCGTACTTAATATTCAAAGGTTATGATATTACGACGCGGTA          | 120 |
| 101 | SerGlyLeuValThrAlaAlaTyrLeuIlePheLysGlyTyrAspIleTyrAspAlaVal          |     |
| 121 | AAGCATGTGAGAACGGTAGTGCCTGGTGTATTGAAAACAGAGGGCAAGCGTTAATGCTT           | 140 |
| 121 | LysHisValArgThrValValProGlyAlaIleGluAsnArgGlyGlnAlaLeuMetLeu          |     |
| 141 | GAGAACTACTATACCCCTGGTCAAAAGTTCAACAGAGAGTGTGCTGAGAGACTACGGGAAG         | 160 |
| 141 | GluAsnTyrThrLeuValLysSerPheAsnArgGluLeuLeuArgAspTyrGlyLys             |     |
| 161 | AAAATTTCACGCTCGGTGACCGAAGGCGGTTCTCCACGCTCTAACGACTCAGTTCAAGACGACTCAGTC | 180 |
| 161 | LysIlePheThrLeuGlyAspProLysAlaValLeuHisAlaSerLysThrThrGlnPhe          |     |
| 181 | ACGATTGAACCTTAAGCAACTTACACGTCAACGAGGCCTTCAATCAGTGCATGGCT              | 200 |
| 181 | ThrIleGluLeuLeuSerAsnLeuHisValAsnGluAlaPheSerIleSerAlaMetAla          |     |
| 201 | CAATCACTGCTCCACTTACGACGTAAGGAGTCTAAACTGAAAGAAGTATTGAA                 | 220 |
| 201 | GlnSerLeuLeuHisPheHisAspValLysValArgSerLysLeuLysGluValPheGlu          |     |
| 221 | AACATGGAATTCTCATCCGCCTCAGAGGAGGTTCTGTCATTATTACCTACTCGATTTC            | 240 |
| 221 | AsnMetGluPheSerSerAlaSerGluValLeuSerPheIleHisLeuLeuAspPhe             |     |
| 241 | TATCAGGATGGCAGGGTTGTTAACCATTTACGATTATCTCCCCGATAGGGTGGATTG             | 260 |
| 241 | TyrGlnAspGlyArgValValLeuThrIleTyrAspTyrLeuProAspArgValAspLeu          |     |
| 261 | ATTTTATTGTGTAAGTGGGTTGTGATAAAATAGTGAAGTCTCGTCTCAGCGAAGAAA             | 280 |
| 261 | IleLeuLeuCysLysTrpGlyCysAspLysIleValGluValSerSerAlaLysLys             |     |
| 281 | ACCGTTGAGAACCTTGAGGAAGAACGGTTCCCTATCCTGGGCTAATTACTTAGACTAT            | 300 |
| 281 | ThrValGluLysLeuValGlyArgLysValSerIleLeuSerTrpAlaAsnTyrLeuAspTyr       |     |
| 301 | GT <sup>TT</sup> TAC  |     |
| 301 | Val End 302   |     |

## FIGURE 12

### *Thermococcus CL-2 Phosphatase (30A1A)* Complete Gene Sequence

ATGAGAATCCTCCTCACCAACGACGACGGCATCTATTCCAACGGTCTGCGCGCGCGGTG  
1 MetArgIleLeuLeuThrAsnAspAspGlyIleTyrSerAsnGlyLeuArgAlaAlaVal 20

AAGGGCCTGAGCGAGCTCGCGAGGTCTACGTCGCCCCGCTCTTCCAGAGGAGCGCG  
21 LysGlyLeuSerGluLeuGlyGluValTyrValValAlaProLeuPheGlnArgSerAla 40

AGCGGTCTGGCGATGACCCCTACACAGGGCGATAAGGGCAAAGAGGGTTGACGTTCCGGC  
41 SerGlyArgAlaMetThrLeuHisArgProIleArgAlaLysArgValAspValProGly 60

GCGAAGATAGCGTATGGCATAGACGGAACGCCGACCGACTGCGTGATTTTGCCATGCC  
61 AlaLysIleAlaTyrGlyIleAspGlyThrProThrAspCysValIlePheAlaIleAla 80

CGCTTCGGCGACTTTGATCTGGCGGTCAAGCGGGATAAAACCTAGGCGAGAACCTGAGCAG  
81 ArgPheGlyAspPheAspLeuAlaValSerGlyIleAsnLeuGlyGluAsnLeuSerThr 100

GAGATAACCGTCTCGGAACGGCCTCGCGGGCGATAGAGGCTTCCACCCACGGGATTCCA  
101 GluIleThrValSerGlyThrAlaSerAlaAlaIleGluAlaSerThrHisGlyIlePro 120

AGTGTAGCTATAAGCCTCGAGGTCGAGTGGAAAGAAGACCCCTCGGCGAGGGGGAGGGTATT  
121 SerValAlaIleSerLeuGluValGluTrpLysLysThrLeuGlyGluGlyIle 140

GACTTCTCGGTTTCAGCACACTCCTGAGAAGGATAGCGACGGCTGTCCTTAAGAAGGGC  
141 AspPheSerValSerAlaHisPheLeuArgArgIleAlaThrAlaValLeuLysGly 160

CTGCCTGAAGGGTGGACATGCTCAACGTGAACGTCCTAGCGACGCCAGCGAGGGACT  
161 LeuProGluGlyValAspMetLeuAsnValAsnValProSerAspAlaSerGluGlyThr 180

GAGATCGCCATAACCGCCTCGCGAGGAAGCGCTATTCTCCGACGATAGAGGAGAGGATA  
181 GluIleAlaIleThrArgLeuAlaArgLysArgTyrSerProThrIleGluGluArgIle 200

GACCCCAAGGGCAACCCCTACTACTGGATCGTTGGCAGGCTCGTCCAGGAGTTGAGCCG  
201 AspProLysGlyAsnProTyrTyrTrpIleValGlyArgLeuValGlnGluPheGluPro 220

GGCACGGACGCCCTACGCTCTGAAAGTCGAGAGAAAGGTCAGCGTCACGCCATAAACATC  
221 GlyThrAspAlaTyrAlaLeuLysValGluArgLysValSerValThrProIleAsnIle 240

GACATGACTGCGAGGGTTGACTTTGAGAACCTTCAAAGGCTCTGAGCCTGTGA  
241 AspMetThrAlaArgValAspPheGluAsnLeuGlnArgLeuLeuSerLeuEnd 258

# FIGURE 13

## *Aquifex VF-5 Phosphatase (34A1A)* Complete Gene Sequence

|     |   |     |
|-----|---|-----|
| 1   | ATGGAAA<br>MetGluAsnLeuLysLysTyrLeuGluValAlaLysIleAlaAlaLeuAlaGlyGln        | 20  |
| 21  | GTTCTGAA<br>ValLeuLysGluAsnPheGlyLysValLysLysGluAsnIleGluGluLysGlyGluLys    | 40  |
| 41  | GACTTGTAA<br>AspPheValSerTyrValAspLysThrSerGluGluArgIleLysGluValIleLeuLys   | 60  |
| 61  | TTCTTCCC<br>PhePheProAspHisGluValValGlyGluGluMetGlyAlaGluGlySerGlySerGlu    | 80  |
| 81  | TACAGGTGG<br>TyrArgTrpPheIleAspProLeuAspGlyThrLysAsnTyrIleAsnGlyPheProIle   | 100 |
| 101 | TTTGCCT<br>PheAlaValSerValGlyLeuValLysGlyGluGluProIleValGlyAlaValTyrLeu     | 120 |
| 121 | CCTTACTTT<br>ProTyrPheAspLysLeuTyrTrpGlyAlaLysGlyLeuGlyAlaTyrValAsnGlyLys   | 140 |
| 141 | AGGATAAAAG<br>ArgIleLysValLysAspAsnGluSerLeuLysHisAlaGlyValValTyrGlyPhePro  | 160 |
| 161 | TCTAGGAGC<br>SerArgSerArgAspIleSerIleTyrLeuAsnIlePheLysAspValPheTyrGlu      | 180 |
| 181 | GTTGGCTCT<br>ValGlySerMetArgArgProGlyAlaAlaValAspLeuCysMetValAlaGluGly      | 200 |
| 201 | ATATTGACGGG<br>IlePheAspGlyMetMetGluPheGluMetLysProTrpAspIleThrAlaGlyLeuVal | 220 |
| 221 | ATACTGAAGGA<br>IleLeuLysGluAlaGlyGlyValTyrThrLeuValGlyGluProPheGlyValSerAsp | 240 |
| 241 | ATAATTGCGGG<br>IleIleAlaGlyAsnLysAlaLeuHisAspPheIleLeuGlnValAlaLysLysTyrMet | 260 |
| 261 | GAAGTGGCGGTGTGA<br>GluValAlaValEnd 265                                      |     |